

## FIGURE 1

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGTCTTCCCG  
CAGCGCTACCGCCATGCGCCTGCCCGCCGGCGCTGGGCTCCTGCCGCTCTGCTG  
CTGCTGCCGCCGGAGGCGCCAAGAACGCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAAACTTGGCGGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA  
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCAGTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCAGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTGCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTCGAACAGAAAC  
GAAGATGCCTGTGCGGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGGAAGACTGTAATGTGCCGGACTTACCCTTAAATTATTCAAGAAGGATGTCC  
CGTGGAAAATGTGGCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATTTGATACTGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGGCCGCACTCTAGAGTGCACCTGCAAGAACAGCAATAGCA  
TCACAAATTCAACAAATAAGCATTCTTCACTGCATTCTAGTTGTGGTTGTCACAAACTC  
ATCAATGTATCTTATCATGCTGGATCGGAATTAATTGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAAGAACCAAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQDGSCRHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGTLNRDCGECEVGWLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGGTGCCTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGC**ATG**CCCAGGAGCGCCTTC  
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCCACTGCAGGGAGGC  
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCCTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCATGTCCCTGTGGAACAGTGCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT  
TCTTAAAACATGTCAACAAGCTGAGTGCCCAGGCCGGTGCAGGAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCAGTGCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCACGATGTATGAATGGTGGACTTGTGTGACTCTGGTTCTGCATCTGCCAACCTG  
GATTCTATGGAGTGAAC TGACAAGCAA ACTGCTCAACCACCTGCTTAATGGAGGACC  
TGTTTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCCCTGCAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTCAAAGCCTGTGCGAGCCTGGCTGGTGCACAT  
GGAACCTGCCATGAACCCAAACAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTGTGAACTTTCA  
TGTGTTGAATGTTCAAATAATGTTATTACACTTAAGAATACTGGCCTGAAATTATTAGCT  
TCATTATAAATCACTGAGCTGATATTACTCTTCCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTGTTCACTGAGCTGCTTGGACAGATTATATTATGTCAATTGA  
TCAGGTTAAAATTCAGTGTGAGTGGCAGATATTCTAAAATTACAATGCATTATGGT  
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAGATATTAGAT  
GTTGTTACATTAAAATTGCTCTTAATTAAACTCTCAATAACATATTGACCT  
TTACCAATTCCAGAGATTCACTGTTAAACAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACCTTTGCAT  
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAACATT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA  
AAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC  
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAI PVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNNGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCNKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICIGKSCKCSKGYQGDLCSPVVC  
EPGCAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCCGGCGGTGCAGAGCCAGGAGGCCAGGGCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACCATGTGGCGATGCCACTGGGCTAC  
TGCTGTTGCTGCCGTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCGTGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCAGGGAGGCCGGTACTGCCAGGA  
GCAGGGACCTGTGCTGCCGGCGTGCACGACTGTGCCCTGCCACTCTGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA  
TCCAGTCTTGGGAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGCATGACCCTGAGGGCATTGCCTACCGCCTGGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGAGCCTTGA  
CCAAGGCAACTGTGCAAGGCTCCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTCT  
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTGATGGTGCTGGTGGTTCTCGCTCG  
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGATGAGGACTTCTCCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGAAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGCC  
CAGCCTGGGCGAGAGGGCCACTTCCGATCGCGCCGTCAATGAGTGCACATCGAG  
AGCTTCGTGCTGGCGTCTGGGCCCGTGGCATGGAGGACATGGTCATCACTGAGGCTG  
CGGGCACACGCGGGTCCGGCTGGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTCGCCGACAGAGGCCGGCGCAGGCCGGCAGGGCCTAAAT  
CCCGCGCGGGTTCCGCTGACGCAAGGCCCTGGAGGCCGGCAGGGCAGGCGAGACTGGCG  
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGGAAGAGCACAGCTGAG  
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATAACCCACCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGTTCA  
AGTGACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC  
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAAGT  
CCTGGCTCAAGCGGTCCACCTGCCTCCCAAAGTGTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTTCACTGTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC  
ALPYLGAIKYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQPQRLLGHDPG

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTCGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCGTCTGCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACGCCACGCCAGTGAGCCTGGG  
AGGCCAGAGAGATACCGCCGGCATGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGA~~T~~CTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACC CGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGA~~A~~CTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGC~~CC~~CAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCAGTGGGAGCCTGTCC~~T~~GGTCC~~T~~GAGGCACATCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCC~~T~~GACCC~~T~~CCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCC~~T~~TAACCCTGTGCTCAGGCACCTCTCCCCAGGAAGCCTT  
CCCTGCCACCC~~T~~ATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCC~~T~~CCCCGCA~~CC~~CAGCA  
GGGGACAGGC~~A~~CTCAGGAGGGCC~~A~~AG~~TAA~~AGGCTGAGATGAAGTGGACTGAGTAGAA~~CT~~TGGA  
GGACAAGAGTCGACGTGAGTTCC~~T~~GGAGTCTCCAGAGATGGGCCTGGAGGC~~T~~GGAGGAA  
GGGCCAGGC~~T~~CACATT~~T~~GTGGGCTCC~~T~~GAATGGCAGCCTGAGCACAGCGTAGGCC~~T~~  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPADFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCCAACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTCAACGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCGCCAGGCTCCGCAGGCCAGAAC  
CAGCGCGAGGCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGCAGTCAGTTGAGTTGTGGCTCCGCCACCGCCGGACCAAGCGCACAC  
GGCGGCCAGGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGCAGGAGATCCCC  
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC  
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGGCCAGCCCCAAACTCCTCTGGTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTAGGAAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCACCTCCTCACATTCCACGCCAGGCCTGCACCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKS KDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCCACATCCAGT  
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACACATTGTATTTAT  
TTCCGTACTCAGAA**ATGGG**CTACAGACCACAAAGTGGCCAGGCATGGGCTTTTCCT  
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGCTCAAACCTCTGGCCTGCC  
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCACAAACAACCAAATTAAATGC  
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGCAAGGAAAAC  
AATATTGACACCATTTCACGGGCTGCTTGCCCAGCTTGAAGCTGAAGAGCTGCACCT  
GGATGACAACCTCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTATTGTTGACAGGAAACCTCCTGACCAACAAGGGTATGCCG  
AGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGTAATTGCTGTCC  
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACAGAT  
AAACACATTCCTTGAACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTCGGGATGCTGACTCAAGGGTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTTCATCTCTCACGTGGGGTTTCACTGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGACCAACGACCCCCGGCCTG  
CCTCTTCAACCCAGCCCCAAGTACAGCTCTCGACCACTCAGCCTCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCTCAAACCTCCTACACATCGAAACTTCCCACGATT  
CTGACTGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTCTATC  
CATTGTAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTCACCCTGATGGCATA  
CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGCACTGTTAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCTGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTAGGAGGC  
CACCAACCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCATCTGGAGATGACAGAAACAGTTCAAGTCAGCTCTCTAAATAACGAT  
CAAACCTTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCAATTAA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACG**TGAC**CAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT  
TTGTCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRNFVYCNERSLTSVPLGIP~~  
EGVT~~VLYLHNNQINNAGFP~~AELHN~~VQSVHTVYLYGNQLDEFPMNLPKNVRLHLQENNIQTI~~  
SRAALAQLLKLEELH~~DDNSISTVGVEDGAFREAI~~SLKLLFLSKNH~~LSSVPVGLPVDLQELR~~  
VDENRIAVI~~SDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLT~~KLKEFSIVRN~~SLSHPPD~~  
LP~~GTHLIRILYLDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNL~~LSNLKQLTARNN  
PWFCDCSIK~~WVTEWLKYIPSSLNVRGFMCGPEQVRGM~~AVRELNMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPN~~PSRSYTPPT~~SKLPTI PDWDGRERVT~~PP~~ISERIQLSIHFVND  
TSIQVSWL~~SLFTVMAYKLTWVKMGHSLVGGIVQERIVSGE~~KQHLSLVNLEPRSTYRICLVPL  
DAFN~~YRAVEDTICSEATTHASYLNNGNTASSHE~~QTTS~~HSMGS~~P~~FLLAGLIGGAVIFV~~LVL  
LSVFCWHMHKKGRY~~TSQWKYNRGRRKDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNN~~DQ~~LLKG~~  
DFRLQPIYTPNGGINYTDCHI P~~NNMRYCNSSVPD~~LEH~~CHT~~

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## **FIGURE 14**

ACTTGGAGCAAGCGGCGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCGCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTGGCGAGGCAGAGGCCAGAGGAAGACCCGGGTGGCTCGCCCGCTGCC  
TCGCTCCCAGGCAGGCCGGCTGCAGCCTGCCCTCTGCTGCCCTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTCCTGCTGATCCTCGGACAGATCGTCCTCCCTGCCAGGGCAGGGCAGGGAGCGGTCACTGGAGAGTT  
CTAGGGGAGACACGCTCGGACCCACCGCAGACGCCCTCTGGAGAGTTCTGTGAGAACACAAGCGGGAGACC  
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTG  
A G C A T C T G C A T T G G A C A T T G G T C T G A T G T C A C C G A G T G G G C T G C T C C A A T G G C A G C A T G T C A A G A A T G  
A G T C T C C C T C A A G A C C T C A A G A G G A A G T C C G A G G T G G A G C G T G C T G C A A G A G G A T G C G G C A T C T G T C C A C C G  
G C A C C A T G A C T G G G C T G G C A T C C A G T A T G C C C T G A C A C A T C G C A T T C A G A A G C A G A G G G G G C C G C C C T G A  
G G G A A T G T G C C A C G G G C T A T A A T G A T C T G C A C A G A T G G G A G A C T C C A G G A C T C C A G G A C G G T G G C T G C T A  
A G G C A C G G G A C A C G G G C A T C C T A A T C T T G C A T T G G C A T T G G C A G G A C T C C A C C T T G A A G T C C A T T G  
G G A G T G A G G C C C A T G A G G A C C A T G T G C A G C A C C T G G A G C A T A C T G T G C C C A C T T C T G C A T C A A C A T C C C T G  
A G A A G A A G T G T G C A C G G G C C A C A T G T G C A G C A C C T G G A G C A T A C T G T G C C C A C T T C T G C A T C A A C A T C C C T G  
G C T C A T C G T C T G C A G G T G C A A A C A A G G C T A C T T C T C A A C T C G G A T C A G A C G A C T T G C A G A A T C C A G G A T C T G T  
G T G C C A T G G A G G A C C A A C T G T G A G C A G C T C T G T G A A T G T G C C G G G C T C T T C G T C T G C C A G T G C T A C A G T G  
G C T A C G C C C T G G C T G A G G A T G G G A A G G G A C T G T G C T G G A C T A C T G T G C C T C A G A A A A C C A C G G A T G T G A A C  
A T G A G T G T G T A A A T G C T G A T G G C T C T A C C T T G C C A G T G C C A T G A A G G A T T T G C T C T T A A C C C A G A T G A A A A A  
C G T C C A A C A G G A T C A A C T A C T G T G C A C T G A C A A C A A C C G G G C T G T G A G G A C A C G T G C T C C G A C G G A G A C G T G T G  
A C T A C T G C C G T G C C A C C G T G G C T A C A C T C T G G A C C C C A T G G C A A A A C C T G C A G C G A G T G G A C C A C T G T G C A C  
A G C A G G A C C A T G G C T G T G A G C A G C T G T G C A A C A C G G A G G A T T C C T C G T C T G C C A G T G C T C A G A A G G C T T C  
T C A T C A A C G A G G A C C T C A A G A C C T G C T C C C G G G T G G A T T A C T G C C T G C T G A G T G A C C A T G G T T G T G A A A T A C T C C T  
G T G C A A C A T G G A C A G A T C C T T G C C T G T C A G T G T C C T G A G G G A C A C G T G C T C C G A C G G A T G G G A A G A C G T G T G  
C A A A T T G G A C T C T T G C T C T G G G G A C C A C G G T T G T G A A C A T T C G T G T G A A G C A G T G A A G A G A T T C G T T G T G  
G C C A G T G C T T G A A G G T T A T A A T C T C G T G A A G A T G G A A A A A C C T G C A G A A G G A A G A T G T C T G C C A A G C T A T A G  
A C C A T G G C T G T G A A C A C A T T T G T G T G A A C A G T G A C G A C T C A T A C A C G T G C G A G T G C T T G G A G G G A T T C C G G C T C  
C T G A G G A T G G G A A A C G T G C C G A A G G A A G G A T G T C T G C A A A T C A A C C A C C A T G G C T G C G A A C A C A T T T G T G T T A  
A T A A T G G G A A T T C C T A C A T C T G C A A A T G C T C A G A G G G A T T T G T T C A G G T G A G G A C G G A A G C G G T G C A A G A A A T  
G C A C T G A A G G C C A A T T G A C C T G G G C T T T G T G A T C G A T G G A T C C A A G A G G T C T G G A G A A G A G A A T T T G A G G T C G  
T G A A G C A G T T G T G C A T G G A A T T A T A G A T T C C T T G A C A A T T T C C C C A A A G C C G C T C G A G T G G G G C T G C T C C A G T  
A T T C C A C A C A G G T C C A C A C A G A G T T C A C T G T G A G G A A C T C A C T G C C A A A G A C A T G A A A A A G C C G T G G C C C  
A C A T G G A A A T A C T G G G A A A G G G C T C A T G A C T G G G G C T C T G A A C A C A C A T G T T G A G G A A G A G T T T A C C C A A G  
G A G A A G G G C C A G G C C C T T C C A A G G G T G C C C A G A G C A G C C A T T G T G T T C A C C G A C G G A C G G G C T C A G G A T G  
A C G T C C G A G T G G G C C A G T A A A G C C A A G G C C A A T G G T A T C A C T A T G T A T G C T G T G T G G G G T A G G A A A A G C C A T T G  
A G G A G G A A C T A C A A G A G A T T G C C T C G A G C C C A C A A C A A G C A T C T C T C A T G C C G A A G A C A T T C A G C A C A A T G G  
A T G A G A T A A G T G A A A A A C T C A A G A A A G G C A T C T G T G A A G C T C T A G A A G A C T C C G A T G G A A G A C A G G A C T C T C C A G  
C A G G G G A C T G C C A A A A C G G T C C A A C A G C C A A C A G A A T C T G A G G C A G T C A C C A T A A A T A T C C A A G A C C T A C T T  
C C T G T T C T A A T T T G C A G T G C A A C A C A G A T A T C T G T T G A A G A A G A C A A T C T T T A C G G T C T A C A C A A A G C T T  
C C C A T T C A A C A A A A C C T C A G G A A G G C C T T T G G A A G A A A A A C A C G A T C A A T G C C A A A T G T G A A A A C C T T A T A T G T  
T C C A G A A C C T T G C C A A A C G A A A G G T A A G A A A A T T A A C A C A G C G C T T A G A A G A A A T G A C A C A G A G A A T G G A A G C C  
T G G A A A A T C G C T G A G A T A C A G A T T G A A G A A A T C C G C A C A C T T G T A G T C A T T G T A T C A C G G A T T A C A A T  
G A A C G C A G T G C A G A G C C C A A A G C T C A G G C T A T T G T T A A T C A A T A A T G T G A A G T A A A A C A T C A G T A C T G A  
G A A A C C T G G G T T T G C C A C A G A A A C A A G A C A A G A A G T A T A C A C T A A T T G T A T A A T T T A T C A G G A A A A A A C C T  
T C A G A A T T C T A A G T G A A T T T A C C A G G T G A G A A T G A A T A A G C T A T G C A A G G T A T T T G T A A T A T A C T G T G G A C A C  
A A C T T G C T T C G C C T C A T C C T G C C T T A G T G T G C A A T C T C A T T G A C T A T A C G A T A A A G T T G C A C A G T C T T A C T T  
C T G T A G A A A C A C T G G C C A T A G G A A A T G C T G T T T T T G T A C T G G A C T T T A C C T T G A T A T A T G T A T A T G G A T G T A T G  
C A T A A A A T C A T A G G A C A T A T G T A C T T G T G G A A C A A G T T G G A T T T T T A T A C A A T A T T A A A A T T C A C C A C T T C A G

## FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGHRARTHPTALLESSCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAVKMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHFCINIPIGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGCEEHECVNMEESYYCRCHRGYTLDPNGKTCRSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCEHSCVSSEDHFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDENLRLSTQKLSHSTKPSGPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGCTCGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCCGTGCCTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC  
**CATG**ATTTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCTCGCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGGCCCAC  
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGCAAGGCCCTGGGAGGCCAGCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**  
CCCACCACTCATTGGCTAAAGGATTGGGTTCTCCTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTGGCTCCAGGC  
CCCCTGATCTGACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGTTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTC  
TTATTAAGACTAACATGAAATATGTGTTGTTCTATTGCAAATTAAATAAGATAACATAA  
TGTTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACNCVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIAPIRTLPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGCGGCCACCGCCA**ATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG**  
TTGAATTGTTCTATACTCAAAATTGCACCAAGACACCTGTCTCCAAATGCAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTG  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTACTAATGATGGAACCCTGCTGTATAGAAAATGTGAATGCAAATGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTACAGAACAAACA  
CTATCTAGCCAAGGGACACCCCTTCTAACTCACTCTTACTGAATTGTAACCCACCGTGAAT  
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTACTGTGAATCATAGGAGAAC  
ACATCTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTTCATCCTCATATGAATATGGATGGAGACTACATAAATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA  
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTCGAATTTCATGTTGCTTCATCTGGTCCTCCATTGGTATTAAAGATTATAATT  
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTGCTTGCCATATGCATTTT  
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAAATCTTGCTG  
TAGCCTATTCTTGCTGAACCTGTTCTTGTGGATCAATACAAATAACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTGATGGATGTGC  
ATTGAAGGCATACATCTCATGTTGTGGGTGTCATCTACAACAAGGGATTTGCA  
CAAGAATTTCATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCAGAACACTTATT  
TGGAGTTTATAGGACCAGCATGCCATAATCATTCTGTTAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAAGAAGTTAGTTGCTTGAGAAC  
TAAGGTCTTGCAAGAGGAGCCCTCGCTCTGTTCTCGGCACCACTGGATCTT  
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTCACAGTCAGCAATGC  
TTTCCAGGGATGTTCATTTTATCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTAAAAATGTCCCCTGTTGGATGTTAAGG**TA****A**ATAGAGAAC  
GTGGATAATTACAACCTGCACAAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAAGTATTAAATCAGTTTCT  
GTTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTAATTAGTTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTTAACACAGAGAAGTATGAA  
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC  
CCTACCACCTCGGTATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACATGAAGGGCAGA  
ATATCAAACAGTGAAGGAAAGGAAATGATAAGATGTATTGAAATGAACACTGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACATTGTGAA  
TTGTTCTGAACCTAAATGTCACAAAAACACTAGACTTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFEVKTVNNFVQRDTFVWDKLSVNHRRTHLTLMHTVEQATLRISQSFKTTEFD  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC  
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCGCAGATCCGAACGGCCTGGGCGGGTCACCCCGGCTGGGA  
CAAGAACGCCGCCCTGCCTGCCGGGGGGAGGGGGCTGGGCTGGGCGGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGTCAAGCAGGAGCGCTCGCTCAGGATCTAGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTCGGCCAGAGCCCCAGGGAGGTGCCATTCGGAGCGGGTGTGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGC  
CCACGTGCACTACGGCTGGGCACCCATCCGCCTGCCGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCAGCTGCTCCTGCGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGGC  
CAGAGCGCCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCACAGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCATTTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACGACAGCATG  
GACCCATTGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT  
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCGGCCCCATTCTGCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC  
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTTAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG  
GCTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAATTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTTGCTGTCCGGTGTACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAGCAGCGGGGAAGACCTAGAAC  
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCCAAATTATATTATGTATGTAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFE  
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES  
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGGCCACCGCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA  
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGC  
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAACT  
CTGCAATTAAACTGTTCCAACTGGACACTGGAGAAATATTCCTGTGAAGCCCGCAATT  
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTGGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAAGAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTACGCCTGTAATCCAGCACTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAAACTTGAACCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA  
AATAAAACTGGTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT  
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSE  
QGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD  
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
SVGYRRCPGKRMQVDDLNIISGIIIAAVVVVA  
LVI  
SVCGLGVCYAQRKG  
YFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA  
AAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTATTAAACATGCTCCACAGCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTCTATGGCATTCA  
TTTGACAAATGCAAGCATTCCCTTATCAATCAGCTCCTATTGAACCTACTAGCACTGACTG  
TGGAACTCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTTCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCTGAAAAATGTCGTCCGAACTGAGCAACTTACAAGAACTCTATATTACACA  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAACAGACATGAACCTTAAGCCTTATCA  
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACAGATAACGCCCTGGT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT  
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACTCTATTAAATAGAA  
TACGAAGGGGTGATTAGCAATATGCTACACTAAAGAGTTGGGATAAAATAATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAAATAGAAC  
TACTAACAAACCTAGATTGCTTACATTCAACCCATGCATTTTCAGACTCCCCAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGAGTCTG  
CCAAACCTCAAGGAAATCAGCATCACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTGCGTGGACC  
CACCTGAATTCCAAGGTAGAAATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGT  
CTCCCTTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT  
TTCCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCATTCTGAGGGAAACACTA  
GATATAAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTGAACTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAAGAGATATTGAGCCATTGAGCTTGGTGTGAAATTCTCA  
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGCAAGACTGAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTACAGAAAAACAGAAAAAA  
TGTGTAATGTCACCAACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAGAATAATAC  
CACAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCCTCTCCAGAAATGAACTGAGCTGATGGTGGACACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCAATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## FIGURE 26

MKDMLPRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYEYSTDFPVNLTGQLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPPLINRLSLVIAGINLTEIPDNAVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPPELISIDS LAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSA LYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHC RATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTL DINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVT KGLHPDQKE  
YEKNNTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGAATCT**  
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAA**CTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT**  
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATGGATTCAAAG  
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCAGATTGCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTGCCATGCTGGTCACCA  
TGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGT**AAGTGTCCAAACTGACTGT**CATTGAGAAAGAAAGAAA  
GTAGTTGGCATTGCACTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTGAA  
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTATTTTT  
AATTAAAAGCAAATAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

## FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCASNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQRLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR  
IQSVHKNAFFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGAACCGAAGGCAGGCCGGAGATGCAGGTGAGCAAGAGGATGCTGGCGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGC  
GGGCTCAGTGTGTCAGGCTGGCCACGGCTGCCGCCCCGCTGCGAGTGCCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGTGCTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACCGCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG  
CTTCCCGCACCTGGAGGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGG  
CCTTCACAAACACTCTCAACCTCCGGACGCTGGGTCTCCGAGCAACGCCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCTCAGCGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCATCCCCACCGAGGCGTGTCCCACCTGCACGCC  
CATCGTCCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCGTCCGCCACCTAGTCTATCTCCGCTTCAACCTCTTACAACCCCCATCA  
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC  
GGGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCCGCGCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCAACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGGTGTTCCGG  
CGCCGCTGGCGCTCAACTCAACCGCAGCAGGCCACGTGCGCCACGCCAGTTGTCCA  
GGGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCC  
CCCGCATCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT  
GTGTGCCGGCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCCACCACTGGCTCATCTTTC  
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGCCCTCATCAGCCAAACAA  
GACCTTCGCTTCATCTCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCCGCCACTG  
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCACTGGCTCATCTTTC  
CTGGCGTGTCTCTGCCTGGTGTGCTGTTCTGGAGCCGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC  
ACGCCTCCGCAAGTTCAACATGAAGATGATATGAAGCCGGGGGGGGCAGGGACCCCCG  
GGCGGCCGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCTCCACCTC  
CTCCCTACCTCTACACACGTTCTTTCTCCCTCCGCCCTCGTCCCTGCTGCC  
CCAGCCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA  
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATT  
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELENENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVRLRLHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDLMTTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNLETLLIDSNPLA  
CDCRLLWVFRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCACCGCGTCCGACCTGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCAGCC  
AGGGAGCCGGCGGGAAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGC  
TGTCGCCTGCTGGCGCCGGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGCTCAAGTCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAAGCCCATCATCACTGGTT  
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTAACAAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
AACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGACACGCCATCATCAATGAGAAGGG  
GGCAGTCAGGAGGGGAGCACAAGAAGGAATATTCATCTAGAGGCGCTGCCACTCCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGCTGC  
TTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTTGAGAAAAGCAAAAAACA  
AACAAAAAACA

## FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCCTTAAACCCTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCTGCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTCTGGGCTGAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATA GACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACCTGCCAAC  
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCCT  
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAACAGAACCTTGCTCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCACACATCCCAGGTCGGTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCAGG  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG  
CTGAGGTCCCTGCCGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCCAGA  
TAGACCTCACGGAAACCCCTGGGAGTGCTCTGCACAAATTGTGCCTTCAAGCAGTGG  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAAGCAGGGTGTCCATCTCGGTGTTGGTCCCAGGACTGCTGCTGGT  
GTTGTCACCTCCGCCCTCACCGTGGGGCATGCTCGTGTGTTACCTGAGGAACCGAAAGC  
GGTCCAAGAGAGCAGAGATGCCAACCTCCCGCGTCCGAGGATTAATTCCCTACAGACAGTCTGT  
GACTCTCCTACTGGCACAAATGGGCCTTACAACGCAAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGAAGGG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGCCCTTGTGACAGAAAGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAFTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPYEEVLEQIPIGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLAPPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANS LPCPGGCSDHIPGSGLKMNCNNRNVS SLADLK  
KLSNVQELFLRDNKIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL  
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLGVFTSAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTCTGTCGCGGCCAAGGGAAACTGTTGGC  
CGCTGGGCCGCGGGGGATTCTTGGCAGTTGGGGTCCCGTCGGAGCGAGGGCGGAGGG  
AAGGGAGGGGGAACCGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCAGACAC  
AGCTCTGCGCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG  
AGA**ATG**AGGGCGGCCTCGCCCTGTGCTCCTCTGGCAGGCGCTCTGGCCCGGGCGGCG  
CGCGAACACCCCCTGCGACCGTGCTGGCTCGGCCTCGGGGCGCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGGCGAGGGCGAGGGCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCAGCTGCGCTGTGCTCGCCTCGAGGGCAGGCCAGG  
GCCCGAGGGGCTCAAAGACCTGCTGTTCTGGTGCACGGCGTCCCCACT  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCCTCCGACCCGGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCAACGGCTACCTGTGCAAGTACCAAGTGTGAGGTCTGTGTCCTGCGCCGCCGG  
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCCAGTCTAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTGGGAGG  
CTTGCCTGGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCGCTTTGTGACCA  
GTGGGAAGGACAGCCGACCCCTGGGGGACGGGGTGCACCAGGCGCCGCCGCG  
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACAGCTGGGAGAGAC  
ACCACTTGCCCTGAACAAGACAATTCAAGTAACATCTATTCCCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCGAGTCAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTCTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCA**AGGAAACAGGGGA**  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACATTAC  
TTGTGTAACTGACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCAGGGAAAAAATAAAAATAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWP GP GGG E HPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACCGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATACTGCCTTAAAAGTCGCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCCGCCCCGGCGGTGCGCGCGTGAAGAGGGAGCGCGGGCAGCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAAGCGGGCGTGTGAAGCGCGTGGGTGCGGA  
GGGGCGTGTGCGCCGGCGCGCGCCGTTGCAAACCCCGAGCGTCACTGCTGCC**ATGA**  
GGGGCGCGAACGCCCTGGCGCCACTCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTAAGTGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTCTGGAGTGTACCTCCAATAGCAAATGTACTTGAAAATCA  
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTTCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGGCCAGCGCATTGGCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTTCAATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACGGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGCTGAGAGAAATGAACCTCTTATTCACT  
TTTATCAGACTTAAGTTAAGTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCTTGTGTCACAAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAAACCATACTCGCGATGGGAGTTG  
CACGCCACAGTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGGCCGG  
CAAGAACATGAGTGCCAGGCTGACTGCGTCTGCAAGCAGTGCCTCTCAGAACAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACAGCTCTGGATGCCTAAAAAATAAGCAATG  
TT**AA**CACTGAACTGTGTCATTAAAGCTGTATTCTGCCATTGCCTTGAAAGATCTATGTT  
TCTCAGTAGAAAAAAATACCTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCACTAGTGCAGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCACATTATTAAGT  
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCAGTTCTA  
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYPAVGTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGVGEDGRGKIMPNSFIMMFTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCCCTGGGGAACAGAGAGGCCCTCGGTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTCAAAAGTTTCTTAATGGTGGTGCCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCTGGTERPCGGYGCCEGEGRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCASFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTACATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCCTTCCAGG  
AGCCGGTCCCCAAGGCCGCCGTGCACAGGCACGGGCCGTGCTCCCGCGCAGGCCCGGGCC  
CGGGTACCGTCGAGTGGCTGCGCGTCCCGCACAGGCACGGGCCGTGCTCCCGCGCAGGCCCGGGCC  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTTCTGGGCCTCGACAGTCGATCGCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGGCCAAGGAGGCTCAGCCATGGCGCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAACCTAATTTGCTCTCAGGAATGAGAATCTTGGCACTGGA  
GAGCCCTGCTCAGTTCTATTACTGACTATATTCTAACGACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCTGTCAC  
TGGATCTGGCTAAAGTCCTCCACCACCTGGAACCTAACGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTATTCT  
AAAA

## FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCCTCGGCGGCTGGTGTCAAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA  
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCAGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT  
GGGATAGTGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCGCCTGTAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTTGAGCCTGGTCGGCTCACCGCTATCATCTGCATTGCCTTACT  
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA  
GTGTTATTCCCCATTTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTGAGCTGGTTCTGGCTTTCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTCCCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTATGCGTGCCCCCACCTGG  
CGCTGCACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCACGGCCA  
CCCAGACTGTCCCAGCAGCGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCAGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCAGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTCAAGCCTGGTACCGCCACCCCTCCTTTGCTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCTGAGGACAAGCAACTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGTGCGGATGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCQTKGQC PPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLA CLAGELRCTLSDDCIPLTWRCGDGH PDCPDSSDELCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCACCGGTCCGGTCTCGCTCGCGCAGCGGGGGCAGCAGAGGTCGCACAGATGCGG  
GTTAGACTGGGGGGGGAGGAGGCGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGATTCCGAGAATGGCTCAGGACCCCCAGCG  
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTGTGATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTTAAACTT  
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGCACTACCTCAAATGGTGAGTCACGGAGATTCGTCT  
GCCACCCGGCCTTGTGAGCGCTACAACCACCGAACTGTGGTGGAGTTACTGCCATCCT  
GGCTACAGCCTCACAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCT  
TTATCAAGTCACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTGGTAGACGGCGTGCCTAGGCCGGTACATGCCCTGTGGCCAG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTAGGCCGGTACATGCCCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTAGGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTTAAAAAATTCCTAAAGTGTCTGAAGTGTCTTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTCTCTTGGTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTTAAAAGNAAAAAA

## FIGURE 48

MYHGMNPSNGDFLEQQQQQQQPSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSODYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## FIGURE 49

CCCACGCGTCCGCTCCGCCCTCCCCCGCCTCCCGTGCAGGTCCGTGGCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCC**ATG**AGGCCGGAACCGCGCTACAGG  
CCGTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGCGCTGAGTGCCTGAGTGC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTTACTTCATGATACTTCTGAAGACTGAACACTTGAGGAAGCCAAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAATTTAGGAACCTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCA  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACATTCATTGCAAATATTCTGATGAGAACCCAGCAGTTCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAACAGATGCCAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGCCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCTCCTGTGGTACCCAGCTAGCACAAAGAACACACCAC  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCAC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAACATTTCAATTCCGAGTGTGTT  
CGGGAGAACCACTCCGATGACATGTCTTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATT**TAG**GACATATAAAAACGAAACTGACAACAATGGAAAAGAAATGATAAGAAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCACGTTGGCTATCCTTAT  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGCTGTGGAGCTTGGAAAACACCTCTGGTGGCTATACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAACATCAAATAAGA  
GCAGGAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL  
VTTVVCWWICRKRKREQPDPSDKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCC CGGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT  
GTT CAGCATGCGCTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT  
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATT CAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACAGAGGCCGGAGGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACTTACCAAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTATACAATG

## FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTIFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACCAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATAACATTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAAACCCAGAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACCGTGGAGTGAA  
GCACCAGAACCAAGTGGTACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCCTCA  
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCAGATGAGACACGTGGTCTGG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAGTCCCTCTCCCTCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGCCGATCTGGCTGGATAATGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCACAGATTGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGCTGCCCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGAACTACATCA  
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCATTGCTCTGGTAAAGGATAAAATTCTGAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTVCQGTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCGGACCGGTGGCGGACCGTGGCGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCC**ATG**GACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT  
GCGGGTGCCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGGA  
TGTGGACAAGAGGGTCAATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCTGCGTGGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAGAGCGGAAATCC  
AAGAACTCC**TAGT**ACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGCTCACAAGTGGG  
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGGTTATTGCAGCTTATAATGGTTAC

## FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTDVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLA AVGKKKDVL IADLLPSL A VYLRT LAPGLF FSLMASRARKERKS KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

## FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKS  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCCCACCGCGTCCGGGACCGCTGGGTGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC  
AGGGAGGAGCACCGACTCGGCCGCACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCTGTGATGCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATAAGAAAGT  
GTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTAACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGCGGCCCTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTTATAACAGTGCACTAATTCACTAGTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACCTTTGCGGT  
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA  
AGATAACAGTACAGTCAGTTAACGCCATGGTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGTGACTTCCATCAGGTAATTATTC  
GAGGGTGGAGGACATATTACCCATGACCAGCCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCTTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTTCTGCAATAAAAATTATCCTGAAACAAGTGGC  
TTTGTGTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTAGGGCTTGAATAGGAAGTTAATTCTCTAAGAGTAAGTGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAAGTAAAAAA

## FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL  
VGPFPGNMKSYAGFLTVDKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCATGTTGGCTACAACAT  
TTTCCTTCTAACAAAGTCTAACAGCTGTCTAACAGCTAGTGATCAGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAATATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTAACATCCTAACAGAGGAGAAAGTATGTTAAAATA  
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGT  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGAAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGCTCTCAGTGGCTGGGTGCTGGCCCCCCCAGCAGCCGGC  
ATGCCTCAGTCAGCACCTTCACTCTGAGAATCGTACTGGACCTAACCAACTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCCTACCAACAATGTCACAAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTTACCCAGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTTACATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGTGAGGA  
TGGCAAGCTTTCATCGGCACGGCTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA  
GCCGGAAGCTGCCGAGACCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTCGCTGCACCCGGG  
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGCCAACGCTGGGACTCACTGGCC  
AGGCCTCAATATCACAGCCAGGACGATGTACTCTTGCCATCTCTCAAAGGGCAGAAG  
CAGTATCACCACCGCCGATGACTCTGCCCTGTGTCCTCCATCCGGGCATCAACTT  
GCAGATCAAGGAGCGCTGCAGTCCTGCTACCGGGCAGGGCACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACCAAGGGCCTGCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCAGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGTCACTGCC  
ATTACACCTCCTCAGCAAAGAGTCCCTTGGAAGGTAAGCTATTGGTGGAGATTAACTATAG  
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTGTG  
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCCAAACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLI IDYSENRLLAGSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMGYGIVRSEGEGDKLFIGTAVDGKQDY  
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFA SGGFVYFL  
TVQ PETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSL A QAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN  
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKE SLLEG SYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCCGCGGGCTGAGTGGACTGGAAACCGGGCCCCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCCTCGCGGAGGCCGGCCGCACGCTGGACTCCTGCTGGCTCTGGGCTTCCTGGCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTCCGTGCCCCAGGGAGTACT  
GGAGGGACGCCGTGCTGAAGATGAAGGCCTGGGCTTGACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTCTCTGGGAACTGGACCTGGAGGCCCTCGCTCTGATGGCGCAGAGATCG  
GGCTGTGGGTGATTCTCGTCCAGGCCCTACATCTGAGTGAGATGGACCTCGGGGCTGCCCAGCTGGCTAC  
TCCAAGACCTGGCATGAGGCTGAGGACAACTTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCACC  
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGCTGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTT CCTATAATAAAGACCCGCATACATGCCCTACGTCAAGAAGGACTGGAGGACCGTGGCATTGGAACTGC  
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCACT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCACCGTCCAGGGACTCAGGCCAAGATGGTATGGAGT  
ACTGGACGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTTGATTCTGTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCCAACACTTGCTCATGAATG  
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGACAGAACGCCGGCG  
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCCTCCCCCACCTG  
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCCTGTACCTGTCTGTGGGACGCCCTCAAGTACC  
TGGGGAGCCAATGCTGAAAAGCCATCAACATGGAGAACCTGCCACTCAATGGGAAATGGACAGTCCT  
TCGGGTACATTCTATGAGGACCGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG  
TGTGTTGTGAACACAGTACATGGGACTTCTGGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGGAGGATCTGGTGGAGAATCGTGGGAGTCAGCTTACACTATGGGAGAATATTGATGACCAGCGAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCTCTGAGGAGACGATGGCGGGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGGAGGAACCACTGAGGTTGGCCTGGACAAATGGNGTTCCCTCCAGAAAACACCCACATTACCTGTTCTTCTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGCGGGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGGAGGAACCACTGAGGTTGGCCTGGACAAATGGNGTTCCCTCCAGAAAACACCCACATTACCTGTTCTTCTGG  
CTCTTGACCTGAAGCCTGGTGGCTGTCGCCCCACCCCTACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAACGCTGCAGGGAAAGGTGGATGGCTCTGGGCC  
TGGTTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCGGAGGCTGTCGGCTGTCTCTAGGGTGGAGC  
AGCTAATCAGATGCCCTGGCCCTCAGAAAAGTGTGAAACGTGCCCTGCACCGGACGTACAGGCC  
TGCAGCATCTGCTGGACTCAGGCGTGTCTTGCTGGTCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCCTCACAAACCTCTGAGCCTCTTGGGATTCTGGAAGGAACCTGGCGTGGAGAAACATGTGACTTCCCTT  
TCCCTTCCACTCGCTGCTTCCACAGGTGACAGGCTGGCTGGAGAAAACAGAAATCCTCACCCCTGGCTCTTCC  
CAAGTTAGCAGGTGTCTGGTGTCTGGTGTGTCAGTGAGCAGGAGGACATGTGAGTCTGGCAGAACGCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGAACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGACATCC  
AGGGAGGAGGAGAACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGACATCCAGGG  
GGAGGAGAACAGAAGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCCATGTCTGACATCCAGGGAGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGAGCAGGCCCTCC  
GAAGTGTGTCAGTCCGATTTGAGCCTGTTCTGGGCCCAGCCAAACACCTGGCTGGCTACTGTCTGA  
GTTGCACTAAAGCTATAACCTTGATCACAA

## **FIGURE 64**

MTTWSLRRR PART LG LLLL VVLGFLV LRR LDW STL VPL RL RQL GLQAK GWN FM LED ST FW  
I FGG SI HY FR VP REY WR DR LL KM KAC GL NT LT TY VP PW NL HE PER GKF DF SGN LD LEAF VL MA  
AE IGL WVI LRP GP YIC SE MDL GG LPS WL LQD PG MRL RT TY KG FT EAV DLY FD HLM SR VV PL Q  
Y KR GG PI IA VQ VEN EY GS YN KDP AY MP YV KKA LE DRG IVE LL TSD NKG LS KG I VQ GV LAT  
IN LQ STHE LQL TT FL FN VQ GT QPK MV MEY WT GW FD SW GG PH NI LD SSE VL KT VSA IVD AGS  
S IN LY MF HG GT NF GFM NGAM HF HDY KSD VT SY DY DAV L TEA GDY TAK YM KL RD FF GS IS GI P  
L PPPP DLL PK MP YE PL TP VL YL SL WD AL KY LGE PI KSE KPI N M EN LP VNG NG QSF GY I LY E  
TS IT SSG ILS GHV HD RGQ VF VNT VSI GFL DY KTT KIA VPL I QGY TV LR IL VEN RG RV NY GEN  
ID DQR KGL I GN LY LN DS PL KNF RI YSL DM KKS FF QRF GLD KWX SL PET PT LPA FF LGS LS IS  
ST PC DT FLK LEG WE KV VF ING QNL GRY WNIG P QKT LY LP GP WL SS GIN QV IV FEET MAG PA  
LQFT ET PHL GRN QY IK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGGCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCT**CCC  
AAGAAGCTGTCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGCTAGTGGATAGGGTCATGACCGGTTCTCTAGACGGGGCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTCTTGGGCCAC  
CGGCTTTGAAGATGCGATGGAGCGGCCAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTGCTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTGCCGAGTGGACTCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGCTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCATTGGCTGGCTCTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGG  
GACTCTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCTGCTT  
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCCTGGATTACTACCACTGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGCATTACTGGCTTCCTAGACTTGCTTGCCCCGTGGCCCAT  
TCATTCAATCTTGCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGTGTGGAGCGAACATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGTTGGGTCTAACAGCAGTGAACCTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGCCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTACGTGCCAAGATCCTGCTGTTCCAGGGAGCCCTCAACAAAATT  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACT**TGAAAGGTAGGCCGGCATGGTGGCTCATGC**  
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACCTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTAAAAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRS FVVRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPhGPLVNSEYYTGWLWQNHSRSVAVTKGLENMLKGASVNMYMFHGKTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWFWPLQLPKWPYPQAPSGPTFSKTFFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTCAGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCCTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTGCTCAAAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCAAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT  
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTACAGTGGCAGTATT  
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGAGGGTTAAGTCATTCAAATCATTGTTTTAAATTGTTGTAACCTGGAT  
AAAGGGAAAGGAAAATTATAACTAAATCTTGGTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCACTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAI FSLSNLQELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTI PPSITHVKNLES LYFSNNKLES LPVAVFSLQ  
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CCACCGCGTCCGGCCTCTCTGGACTTGACATTGCATTCCATTCTTCAAGACAAACTGACTTTTTATTC  
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGCATTGCTTAGTGGTTGTGAGGGAGGACACGTGG  
GCTCAGTGCTTGCTGCACCTATGCCTAGGTACATGAAGTCTTGACCTACAGTGATTATGCCTGTC  
ATCGCTGGTGGTACCTGGCCCTGCTCTGCTGATAGTTGCTGCTCTGCTTACTTCAAACACAAAC  
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGGCTGAAAAAATCACACCCAGACAAGGTGTGGTGGCCAAG  
AACAGCCAGGCCAAACCATTGCCACGGAGCTGTGCTGCCCTGCAGTGAGGATATAGAATGTGTC  
AGTTTGATTCCCTGCCACCTTGCTGTCAGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGAGGCACAGAAGAAAGGCACAG  
CTCCCCCATGTTCATGAAAATAACTCAGTGCTGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCCCTTCAGGAAGGAGTTGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAAACAGTC  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCTGGACTGACGTTCCCTGGAGGTGTCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCTCTAAGGCTGCCAGGCCCTGCCAAA**ATGAGCTTGT**  
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGGGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGTGCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT  
GATCCAGATGAAAGCTGAAAGTGAAAACATAAAGTCTTGACGGAACCTCAGCAATGGGCCTGCTAGGG  
CAAGTCTGAGTAAAACGACTATGTTCTGATTTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGCTTTCTACTACTTCTCTCTTAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAAAGGATCCTTCACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAAGATTACAAGATAAAACTAACTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT  
GGCGTGTGACTCCCACCTTCGAATCGTCAACTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGGATTCTGCTCCTACACCTCAATTATGCAAGAAACATCAACACTACATCTTAACTTGCTCTCT  
GACAGGATGAGAGTATTATAAGCAAATCCTACCTAGAGGTTTAACTCTAAAGGATAACTGCAACTAAA  
GACCCAACCTGAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTCTAATGGATGTTGACAATCAGA  
AAGGTAGAAGATCAGTCAATTACACCAATATAATCACCTTCTGCATCTCAACTCTGAAGTGTACCC  
CGTCAGAAACAACCTCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACAA  
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATAACACCGCATGGCTTTTGAAATCCAATTCA  
TTTGGAAAAGACTATACTTGAAATCACCATTATGTGGATTGAAACCAACTCTTGTCAAGTTAGTCTGCAC  
ACCTCAGATCAAATTGTTGGGTCTTCTGATACCTGTAAGGCTCTCCACCTCTGACTTTGCATCTCAAACC  
TACGACCTAATCAAGAGTGGATGTAAGTGCAGAGTGAAACTGTAAAGGTGATCCCTTATTGGACACTATGGGAGA  
TTCCAGTTAACGCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCAGTGTAAAGTTGATATGTGAT  
AGCAGTGACCAACAGTCTGCTGCAATCAAGGTTGTCCTCAGAACAGAAACGGAGACATTCTCATATAATGG  
AAAACAGATTCCATCATGGACCCATTGCTGAAAAGGGATGCAAGTGCAAGTGGCAATTAGGATTTGAGCAT  
GAAACACATGCCAGAAACTCAAACCGCCCTCAACAGTGTGCACTGTTCTCATGGTTAGCTCTG  
AATGTGGTGAACAGTGTAGCGACAATCACAGTGAGGCATTGAAATCAACGGGAGACTACAAATACCAAGAGCTG  
CAGAACTATT**AA**ACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGTCACCTCGT  
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCATGTA

## **FIGURE 70**

MELVRRLMPLTLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSPVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYWKTDIIGPIRLKDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGGACAGCCGGCCTGCGCCG  
GGAC**AT**GCAGGCCAGGAGCTCCCAGGCTCGCGTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCCTCGACCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG  
GGGAGTGTTCGCCCAGCTCGTAGCGAGTGGTCTGGTGGATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTGGACCACTATTACAGAAAATTTTAATGCCAACAGTGGGAGATATTTCAGGC  
CTCTGGTCCAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT  
CAGAATATTGGAACTGGAATGCCATAGATGAGGGCCAAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACCTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTCCAG  
TTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGACACGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA  
CATAAATGGAAAAGTGCATGACAATAGACAAACTGTCTGGGCTATAGGAGGGAAAGCTGG  
AATCTCTGACTATCTACAAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC TG  
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC  
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATC**TAA**AGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTCAGCCCTTCCCTTTCCACTA  
AATTTCCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAAGTAAAATTATGTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATCTGTAAAATGGTCACCTGTATAGGGCACTTACCAAGCAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA  
GTTTTCTTCTCAATTATAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSPKPEKLVYAIIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCCAAGGCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCACTGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACCGAC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA  
TGGATTCTGGTGTCACTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTG  
TCCTGATTGGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATGAT  
ACTTGGACTAACTCGCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA  
AACTGCAACACAAACAGAATTATTGTCAAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAAGCTGGTCTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCC  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCTAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCACCC  
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAC  
CCTTCTCCTTATTGTAACCCCTGTCTGATCCTATCCTCTACCTCCAAAGCTCC  
TTTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAAAGGAGTTTGCAAGTGAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC  
CCTTCTCAGCTGAAAGAGAACACGTATCCCACCTGACATGCTCTGAGCCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTGTTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATATACTTTACAAGTAACAAAAAATAAAACCTTATAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCT  
GTTTGATATTCTAGCTTACTCTCAAACATAATTCTATTCTGAGACTAATCTT  
ATTCATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACACACCAAG  
TACATTGTTACCTCTATATACCAAGCACATTAAAAGTGCCTTAACAAATGTACT  
GCCCTCTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAYCYNSSDTWNTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAALKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCCGACTTCACGATGG  
CTCGCCCAACCTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGTATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTATGGACCTCTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA  
TGGGGAAAACAAGAAGGATAAATAAGATCCTCAGTTGGCAGTGCTTCTCCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGCCACTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTACTGCTTATC  
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTT  
TTGACCTGCACAGCTTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCCCCAAGGACTCTGCTTCAAGCCCTCTGGCTTGTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG  
TTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTGAGACTTCCCTTGTGTGGTAGGACTTGGAGGAGAAACCCCTGGACTTCAC  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDI RMGLLYITLCIVFL  
MTCKPPL YMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNI PEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**A****T**GATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGAC  
GGCGACGGCTGGGTGCGCTGGCGAGCTCGCGTGGATCGCGCACACGCAGCAGCGGA  
CATACGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCCACCGCGCTGGATGGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGCGTTCCGGTGGC  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTAACGCCAGCCTGGGAGGA  
GGAGCCGGCGTGGTGAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGCCC  
CTGGTGGAAGCCAACCAACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCT**G****A****C**CGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAATGACGGAGGAGGGGCCGTGGTCTGGCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCTGTACACCCCCAACCCCAAGGGAGGGCTGTATAGTCCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCAGCCAGCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT  
GGCCCCAGCCCTCTCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDRDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLRNKGYVQVEEYIADLYSAEPGEEPAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GC GGCGGGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTCGCTCCCAG  
CCTGTCTGTCGTTGGCGCCCCGCCTCCCGCGGTGCAGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGCCGCGAGGCCTCCAGACCTAGAGGGCGCTGGCTGGAGCAG  
CGGGTCGTCTGTCTCTCTCGGCCGCCCGGGATCCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACGCAGGGCCTCCGCACCCCTGGCCTGCCGATTCTCCCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCGGCTCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACAGAGGCTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATA  
GGCGAGAAAATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAA  
CAATAAGAGATTGAAAGCAGACATTGCATTCTGATTGATGGAGCTTAAATATTGGCAGC  
GCCGATTTAACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATT  
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA  
GTAAGAAAAGGATCCCCAAAGTGGTGGTGGTATTGATGGCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT  
CAGTGAACATTGCCCTTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC  
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGGCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTGTTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCA  
AGAACCATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGATT  
CTCATAATACTGAAATGCTTCTGATCAGTAAAGCAGATACAAAATATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCGCGCTCCGCACCCGGGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGAACTCGGTCCAGTCG  
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCTGCTGTGCCTGC  
TGCTGGCGCGGGCTCCACGGCCCCCGCGCCGCTCCGACGGCAGCTCGGCTCCAGTC  
AAGCCGGCCGGCTCTCAGCTACCCGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG  
CAGAAGAACGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATGCCAGGAGAAAT  
TCACAAGATAACCAACAAACAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGAGACGAAGAAGGCAGAAGGAGCAGAGTCATCGACGAGGACTGTGGGCCAGC  
ATGTAUTGCCAGTTGCCAGCTTCACTACACCTGCCAGCCATGCCAGGGCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA  
GCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCTCCTGCAAGCCCCACAGCCACAGCCTG  
GTGTATGTGCAAGCCACCTCGTGGGGAGCCGTACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTCATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCT  
GCACTGCTGGAGGGAAAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA  
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTCATTGTTCA  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTTGCCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACCGAGTTCTTCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACTACATGTTTATTCA  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCA  
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTGGTGCCACCAA  
AAAGTGTCCCCAAAAGGAAGGAGAATGGATTTTCTTGAGGCATGCACATCTGGAATTAG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGAGCCGTCTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT  
TGCATTAGTAACATTGAAAGGTATATGACTGAGCGTAGCATAAGGTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC  
TGAAGACAATTATCACCAACAGTGGAGAAAATCAAACCGAGCAGGGCTGTTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTGACAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAGAAATCAAGC  
ATAAAACTCACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASCGLLQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTCCTCCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCCTGCCATTACCTCTGCAGCTCTGGCTTGAGTCAAAAACATGGGAGGG  
CCAGGCACGGTCACTCACACCTGTAATCCCAGCATTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG  
TTCGAGACCAGCCTGCCAACATGGAGAAACCCCCATCTCTACTAAAATACAAAAATTAGCCAGGAGTGGTGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGGCCAGGAGAATCGCTGTAATCCAGGAGGCCAGGATGCAGT  
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGTGCAGAATGAGACTCTGTCTCAAACAAACACACGGGAGGA  
GGGGTAGATACTGCTCTGCAACCTCCTTAACCTGATCCTCTTCCAGGGCTGCCCTGATGGGCTG  
GCAATGACTGAGCAGGCCAGAGGACAGGAAAGGAGAAGGCATATTGAGGAGGGCAAGAAGTGAACGCCCG  
GTGAGAATGACTGCCCTGGGAGGGTCTTGGGAGGGTGGCTGACCCCTACCCCTGCAATGTTCCCTGCCCTCA  
AAGAGCAGGACTCCAGACTCTCTTGTAATGGTCCCTGCCACTGCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTCA  
ACTCTGCTAGCTTGGGTGGCTGGCACTGCCACTGCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTCA  
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTCCTACCGCAGGCTACCCACTGTGGACTGCAATGA  
CCTATTCCCTGACGGCAGTCCCCCGGCACTCCCCGCAAGCACACAGACCCCTGCTGCAAGAGCAACAGCATTG  
CCGTGAGGACAGTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT  
TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT  
GGAGGACACAGCTTGCAAGGCTGGCAGCCATAGGAACCTATCTCAACACCACACCAGCTACCGCATTGC  
CCCCAGGGCCTTCTGCCCTCAGCAACTTGTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACTGGAGACTCATGATTGGGGCAACAAAGGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCTGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCGACTATGC  
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCTATGACAACCAGCTGCCCGGGTGCCTAGGGCAGGACT  
GGAACAGGTGCCGGCTCAAGTTCTAGACCTCAACAAGAACCCCTCAGCGGGTAGGGCGGGGACTTGC  
CAACATGCTGACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGCTCCATGACAAGTTGCCCTG  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGCTCCTCATCCACCCCGCGCCTTCA  
CCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAAACACGCTCTCAGTGCCTGCACAGCAGACGGTGGAGTC  
CCTGCCCAACCTGCAAGGAGTAGGCTCTCCACGGCAACCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC  
CACGGGCAACCGTGTCCACGGCAATCCACCCCTGTGCGGAGCTCCAGCAGACGGTGGAGTC  
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACCATGTTGCCCTCATCTCCCCAGGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCGAACCCGAACCCAGAGATCTACTG  
GGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAAGGAGGTACCCGGTGTACCCGAGGGGACCT  
GGAGCTGCCAGGGTGACAGCAGAACAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCTCCAGCCAGGAGGGACAGGGAGACAGGGCTGGAGCTCG  
GGTCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTCAACCCACCCAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCTCCCTCCGGGCCAGGGGCCACAGCTGGCCCGCTGCCTGGGAACCCACAGCTA  
CAACATTACCCGCTCTCAGGCCACGGAGTACTGGGCTGCCGTGCAAGTGGCCTTGCTGATGCCACACCA  
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTCTTGCCACAGAGCCTAGGGGATGTCCTGGCTCAT  
TGCCATCCTGGCTCTGCTGTGCTCTCTGGCAGCTGGCTAGGGCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGAGGCGGCCTCTCCCTCAGCCTGGGTTCTGGGCTGGAGTGCCTCTGTGTCGGGTG  
GTCTGCTCCCTCGTCCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC  
ACCATTGTCTCAAATTCTGAAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA  
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAGGACATGGACCCACGTGCTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGGTTTGTGGCCCTGGGGTGTCTGCAAGCCTGAAAAAGTTGCCCTACCTCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCTGCCCTCCCATCTT  
CTCTCTGCTGCCAGGGCTCTGGCTGGCTTCTGCCCCACCTGTGCTGCCCCGGGCTGCACCCCTTCCCTCTC  
TCTTCTCTGCTACAGTCTGCTGCTCTGTGCTCTGGCACAGGAGGGCTGAAGGAGGCCACTCCATCTCAC  
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA  
CGCCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGAAATTGTACCTTGTGGAGAA  
ATGTGTCACCTCCCCAACCGATTCACTCTTCTCTGTTGAAAAAATAAAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQEELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANRSLVLAGMNLRREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGKLFDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMELTMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGDADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPPNTVSTNLTW  
SSASSLRGQQATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRRLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC  
CCTGCCACACTCTCAAGATCCTGGCGTCCTCTACATCAGCCTAGTCATCTCTACGCCCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGACCTCATTGACCAAATCGACCCGCTACTCCAA  
GCGCTTCGCCGTCTCTGCGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTACCAAGAACCGCAGGACAAGCTGGAGCTGACCTGTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCAGCTGACCATCCCGCC  
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTTACCAACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACACCGCTACATCGTCATCGA  
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAACGCAAGCTGCCACAGGTGGTCA  
AGATGTGGCGTGCACCTGCAGAACGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCATCTTCAGCCT  
CCACAACCTGCAAGGAGATTGACCTCAAGGACAACAAACCTCAAGAACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCCTAACGCTGTTAACACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGGCCCTCTACCTGAAACCGAACAAAGATCGAGAACAGATCCCCACCCAGCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACACCTGACCTTCCCTGCCGACATCGCCTCCTGCGAGAACCTCCAGAACCT  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCGGG  
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCTCAGGCCGGAGGGCAGGCCAGCTCTCCAG  
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGGAGCTGGGGCGCTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGTGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCAGGGCTGAG  
CTGCCACCAGAGGTCTGGACCCCTCACTTTAGTTCTGGTATTATTTCTCCATCTCCACCTCCTTCATCC  
AGATAACTTATACATTCCAAGAAAGTTAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTCCCC  
TTGTCCTTATTAGCGATGCCGCCGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGCGAACAG  
CCATGGGACGGTCACCCAGCAGTGCCGGCTGGCTCTCGCGTGCAGTCCACGGGAGAGCAGGCCAGCTGG  
AAGGCCAGGCCCTGGAGCTGCCCTCAGTTTGTTGTGGCAGTTAGTTAGTTAGTTAGTTAGTTAGTT  
AAACAATTTTTAAAAAAAAGCTTGAAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTAAAAAAA  
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAGGCCAGACGT  
TGAAGTGTGTTCTCTTCCCTGGGGAGGGAGGTTTTGTGTTTTGGGTTTTGGTGTCTGTTCTTCTCCT  
CTATTGTTCTGGCAGGCACTCATTTCTGTGGCTGTCGGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGGATGAAACGGTGCTCCATTGCACCTCCCTCCTGCGCTGCCCTGCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCCTGCCAGGGTGT  
CCAGTGCCACCGCTGCCCTCGCTGCTTCCATCAGCCCTGCGCACCTGGTCTTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGGAGGTGGCAGGGCAGGGTGGCTGGTCCAGGCCAGGGTCCCTGGCC  
CTGGAGTGCACACAGCCCAGTGGCACCTGGTGGCTGGAGGCCAACCTGCTTAGATCACTCGGGTCCCCACCT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCGTCCATTGTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA  
ATCTATAACAGAAAAAA

## **FIGURE 88**

MRQTI IKVIKFILII CYTVYYVHN IKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNLNEWTLDKLRQRLTKNAQDKLELHLMGLSGIPDTVFVLDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENRLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGEITNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTCCATTCTACATTTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCAGGGGGT  
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTCGAACGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTGACATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG  
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTT  
TACTGGATTCTGAAAGCTGGTCATATGGTTCCCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAUCAAGAATTAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLGlnAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCATCGTGGTGAGAGGACGCCAAGTCACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAAACCTATACTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATATAAACAA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTCAGTGGACTCAGGTGGACCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCACTACTCTTTCCCTCT  
TCTCTGGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

## FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCACGGCTCCGGGACCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCTGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG  
CTCTCCTCAATAACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGANGCCATCCC  
CACTGACCCCTCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCTGTGATCCGTAAAGCATAACTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT  
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGGCCCTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCAACCTCCCTGCCCTCAG  
CCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACGCCACATCCAGTTACTTCATG  
CAGTGGCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCTCTGGCTTCTCAACCCAAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTGTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCAGCTTGTTGAAGACTCTACTCAACCCCTGACCCCTTCCTATC  
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTTCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA  
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCCCTACTTAGCTCCAGGTCTTAACCTCTCTG  
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC  
TCCATTGAGATTGCTTCTCAGTTACTCATGCTCCCTGGAAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVA\_DLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSQLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP  
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GGGCTGCTCGCGCGAACAGTGTGCTGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC  
GCCTGCATAACGCCCTCCCTGTCGTCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTTCAATGTGGACCCCAGTGTGTCATAAGGGAAC  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA  
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCAGAATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATGCTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGCGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAATTATTGGCATTTCAGG  
GCACCACTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAGATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGTCCCTCCTGGCAGCAATTAGGGCTTCAATGTTCTTATTAGGAGAGGCC  
AAATTGTTTTGTCATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG  
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAATCTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTGT  
CAAACTTGATTTATTCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## FIGURE 96

MAGIPGLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGD  
GAQHRDGS  
GGKS  
RRKRQIYGYDSRFSIFGKDPLLNP  
FSTSVKLSTGCTGTLVAEKHVLTA  
AAHC  
IHDGKTYVKG  
TQKLRVGFLPKFKDGGRGANDSTS  
SAMPEQM  
KFQWIRVKRTHVPKG  
WI  
GNANDIGMDYDYA  
LLELKPKH  
RKFMKIGV  
SPPAKQLPG  
GRIHFSGYDND  
RPGNLVYRFCDV  
KDETYD  
LLYQQCD  
AQPGASGSGVYV  
RMWKRQQQKWER  
KIIGIFSGH  
QWDMNGSPQDFN  
AVRITPLKYA  
QICYW  
IKGNYLD  
CREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGTCTCTCGAGCCTGCTGCCGTCCCCCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTTGGAAAGCCCCA  
GCAGCTGAACC GGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGTGTTGCCTGGGTGGAGC  
CCCACCCCTGTGTATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCGACTCGGAAGTCTGCAGCCAT  
CTGTA C TGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGAGC  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGTCTACATCAGCCTCTCGCGCACCGCTCTGGGTGGAGAAGATCGTCAAGGGTGCA  
GCTCCCGGGCGCCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC  
CCCGCGCTCCTAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGCCAGATCCACA  
TCTGGATCTGGATCTCGGGCGCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAAACCTGCCACATATCTTATTATTCCCTCCAATTCAATAAATTATTTATT  
CTCCAAAAAAA

## FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPI CLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGGAGTC  
GGCTGTGGTTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCCTCCAATGTCCCTCTGGCTACCAACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGTGGAAACCCAGGCC  
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC  
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGTCATGTGTGGGCCCTCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATAACCAACTCAAAGGG  
TGAAGAGGTCA GCTGTCCTCTGTCA TCTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTCT  
TTTGAGTGGGGAGGCAGGGACGAGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGNKMERGRGENLFAITDEGMDVPLAMEEWHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTVPSPENSLDPKMSLTGARELLPHAQEEAEAAELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTA ACT GAG TCA GGG CTT TCAT TGG GAG CCC CCT CAAC AGA ATT CGG TCA TT CCA AGT T **A**T GGT GG ACG T  
ACT TCT GTT GTC CCCC TGCT TTT ACATT AGCAG ACC GG ACT TAAGT CACA CAG ATT AT CTT CAT  
CAAGG CAAG TCC ATG AGC CAC CT CAAG CTT CGAG AAGT GAAC AA CAA AT GAATT GGAG ACC ATT CC  
AAAT CTGGG ACC AGT CTC CGC AAAT ATT AC ACT TCT CTC CT GGCT GGAA ACAGG ATT GTT GAA AT ACT CCCC TG  
ACAT CTGAA AGAG TTT CAG TCC CTGAA ACT TT GGAC CT TAG CAG CAAC AA TATT CAG AGC TCC AA ACT GCATT  
TCC AGC CCT ACAG CT CAAT AT CTG TAT CT CAAC AGC ACC GAG TCA GCT ACAT CAAT GGAA CCT GG TATT TGACAA  
TTTGCCA ACAC ACT CCCC TGTT AAAG CTGAAC AGGAA ACAAG ATT AAAA AT GTAG AT GGACT GAC ATT CCAGG CCTT GG  
GCC CA ACT GCA AC AT CTG AAT TGAA CC GA ACAAG ATT AAAA AT GTAG AT GGACT GAC ATT CCAGG CCTT GG  
TGCT CTGAA GTCT CTGAAA AT GCAA AGA AT GGAG TAAC GAA ACT TAT GGAT GGAG CTTT GGGG CTGAG CAA  
CATGGAA ATT TGCA GCT GGACC ATAACA CCTAACAGAG ATT ACCAAAGG CTGGCTTACGGCTTGCATGCT  
GCAGGAAC TT CAT CTG CCAAA ATGCC AT CAAC AGGAT CAG CCTGAT GCTGGGAGTCTGCCAGAAGCTCAG  
TGAGCTGGAC TAACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCTGGCCTAAGCTTACTAAATAC  
ACTGCACATTGGGAAACAACAGAGTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGT TAAAGACTTT  
GGATCTGAAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTC TTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT  
GCATT TAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTT  
TCAGAGCTTGTAAATGCCAGTTGCCCCATCCTCAGCTGCTAAAGGAAAGCAGTGGCTTAGCCAGA  
TGGCTTGTGAGT GATGATT TCC CAAACCCAGATCACGGTT CAGCCAGAAACACAGTGGCAATAAAAGGTT  
CAATT TGAGTTCATCTGCTCAGCTGCCAGCAGT GATGCTTCCCAATGACTTTGCTTGAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGGTATGGAGTATACAC  
CATCCTCGGCTGGCGAGGTGGAATTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCAATCATTGGTTC  
ATCCTACTCTGCTAAAGCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACC  
CCGAGCTGGGCCATGGCACGCTGGAGTGCTGCTGTGGGACCCAGCCCCCAGATAGCCTGCCAGAAGGA  
TGGGGCACAGACTTCCAGCTGCA CGGGAGAGACGCATGCTGATGCTGGAGGATGACGTGTTCTTATCGT  
GGATGTGAA GATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC  
AACTCTGACTGTCCTAGAAACACCATCATT TGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGC  
CGT CCTACAGTGCATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAAC TGACCAAAAGATGATAGCCCATTGGTGG  
AACCGAGAGGACTTTTGCA CGCAGGAATCAGCTCTGATTATGTGGACTCAGATGTCA GTGCTGGAA  
ATACACATGTGAGATGCTAACACCC TTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCAC TCAAC  
CTGC GACT CCC CT CAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGTGTGTCATAGC  
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGTCA TCA TACACACAAGGCGGAGGAATGAAGA  
TTG CAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATGTCA TCTCAGGGAAACGTT  
AGCTGACAGG CAGGATGGTACGTGCTT CAGAAAGTGGAGCCACCACAGTTGTCA CATCTCAGGTGCTGG  
ATT TTTCTTACCAACACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC  
CACAGATCTGCTTGTGGGGATCCACAGGCCATATTGACAAGTGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTGCA GTGCTGACCTAGATGCCATTCTCAGAAGAATCCTGCGAACGGAGCTTCA  
CATAAAGAAAAGGAGT GCTACCCATGTTCTCATCCTCAGAAGAATCCTGCGAACGGAGCTTCA  
GTGCCCTCACATGTGAGGAAGCTACTTAAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGT  
TCTAAACAAGTCTCTTGTGAAAGCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGC  
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGC  
AAGAGCCTTATTGAAAGCTCATTCTCCCAGACTTGGACTCTGGTCA GAGGAAGATGGAAAGAAAGGAC  
AGATTT CAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAGTC  
TTATGACTTGAGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAAC  
AAAGAGAGAGAATCTTATGTTTAAATGGAGTTATGAATT TAAAGGATAAAAATGCTTATTATACAGAT  
GAACCAAATTAACAAAAGTTATGAAAATT TACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA  
TTTTTTAACTTGT TATGCA AAAAAGTATCTTACGTAATTATGATATAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCA  
TTAAATAGAAGTTACTCATTATTTGCACATTATTTAATAAAATGTGCAATTGAA

## **FIGURE 102**

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAGQ  
GEVMEYTTIIRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHGPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCQAQN  
SAGSISANATLVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTER  
HFFAAGNQLLIIVDSDVS DAGKYTC EMSNTLGTERGNVRLSVIPTPTCDSPQM TAPS LDDDG  
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGT LAD  
RQDG YVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGS DP FETYHTGCSPDPRTVLM DHYEPSYIKK ECP CSHPSE ESCER SFN ISW  
PSHVRKLLNTSY SHNEGPGMKNLCLNKS LDFS ANPEP AVASSNS FMGT FGK ALRRPHLDA  
YSSFGQPSDCQPR AFYLKAHSSPD LGSEEDG KERTDF QEE NHIC TFK QTLEN YRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGTGCCTTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGGGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTTCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGACGTTGGATTCTCATCAACCTCCTTTTTAAAT  
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC  
GCTGGCTCTCACTTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCTGCAGCAA  
CCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTGCGTGAGGTCCGGATGGCATCTCCACCAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGCTTGAGGCACATTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCCATTGAAATTGGGGCTTTCAATGGTCTGGCAACCTCAACACTTGGA  
ACTCTTGACAAATCGTCTTACTACCATCCCAGAACATTGAGCTTGTATACTTGCTTAAACTGAAGGAGCTCTGGT  
GGCAAACAACCCATTGAAAGCATCCCTCTGTTAACAGAAATTCTCTTGGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC  
CATGTGAAACCTTCGGAAATCCCTAACCTCACACCGCTCATAAAACACTAGATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCTCCAGAT  
TCAAGTGAACGGAATGCCATTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCATGACCTCTCACTCCCTGCATCATCTAGAGCGATACATTACATCACAACCCCTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGCCCCGGT  
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGCCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGGTACAAAGTGCAGTAGCTGT  
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACCTGTGCAAGATAAGGCATGTACACATGTATGGTGAGTAA  
TTCCGGTGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCAAGCAACCAACTCTTCTCTTACTTT  
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACCACAGATAACAAATGTGGGTCCCACCTC  
AGTGGTCAGTGGAGACCAATGTGACCACTCTCACACCCACAGAGCACAGGTGACAGAGAAAACCTT  
CACCATCCCAGTGAATGATGAAACTGGGATCCCAGGAATTGATGAGGTGATGAGACTACAAAATCATCAT  
TGGGTGTTGTGGCCATCACACTCATGGCTCAGTGAAATTATTAATGTTGATGAGGATGAGGAAAGCAGCACCA  
TCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAATGTTGATGAGGATGAGGAAAGCAGCACCA  
CATGGAAAGCCACCTGCCATGCCTGCTATCGACCATGAGGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACACACAAACAGTTAACACAATAATTCAATACACAGTTGCACTGATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATTAAAACATTACAGAGTTACAAAAAAACAAACAAATCAAAAAAA  
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAATTATTATTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCIDIL  
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN  
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAAACCTCTGTTGAGTTGGCAGTTCTTTCGGTTTCCCTCTGCTGTTGGGGCA  
TGAAAGGGCTCGCCGCCGGAGTAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGACCGCACCGC  
GAGGGCGGGCGTGCACCCCTGGCTGGAAGTTGTGCCGGGCCCGAGCGCGCCGGCTGGAGCTCGGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCGTGCCGCCGGACTCGGGCAGCCCTCTGGGTAGCGCC  
GCGGTGCTGGGCGCGTGGCGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGTAGCGCC  
GAGGCCCATGCCCCACTACCTGCCGCTGCCCTGGGACCTGCTGAGTCAGTCGAAGCGGCTAGCGCTT  
CCCAGGCCACTCCCGTCTGGCTCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC  
ATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACAATGAATTGGAGACCATTCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACTTGGACCTAGCAGCAACAATATTCAAGAGCTCCAAACTGCAATTCCAGCCCTACAG  
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAATTGCCAACACA  
CTCCTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAACTGCCAACACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCCTGGTCTGAAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAATTTG  
CAGCTGGACCATAACACCTAACAGAGATTACCAAGGGCTGGCTTACGGCTTGTGATGCTGAGCAACTTCAAT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGGACTGCCAGAAAGCTCAGTGAGCTGGACCTA  
ACTTCATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCTTAAGCTTAAACTAACACTGCAATTGGG  
AACAAACAGAGTCAGTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC  
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGCTTACGAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGGTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTACAAGGCAATGCAATTCAAAATGAAGAAACTGCAACAAATTGCAATTAAATACA  
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAATTTCAGAGCTTGT  
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCCAGATGGCTTGT  
GATGATTTCCTAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTCAATTGAGTT  
ATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCAATGACTTTGCTGGAAAAAGACAATGAAACTGCA  
GCTGAAATGAAAATTATGCAACACTCCGGGCCAAGGTGGCGAGGTGATGGAGTACCACTCCTGGCTG  
CGCAGGGTGGAAATTGCCAGTGAAGGGAAATACAGTGTGTCATCTCAACTTGGTTCATCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCAACAGACCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCACGCTGGAGTGTGCTGCTGTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTGCACGGAGAGACGCATGATGCCAGGATGACGTGTTCTTATGTTGAGATA  
GAGGACATTGGGTATACAGCTGCACAGTCAGAACAGTCAGGAGTATTTCAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATATTGCGGGCACTGTGGACCGAAACTGTAACCAAGGGAGAACAGCCGTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACAAAGATAGCCATTGGTGTGTAACCGAGAGGAC  
TTTTTGCAAGCAGGAATCAGCTTGTGATTATTGTGGACTCAGATGTCAGTGTGATGCTGGAAATA  
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCACCTCAACCTGCA  
CAGATGACAGCCCCATGTTAGACGATGACGGATGGGCACTGTGGGTGTCGTGATCATAGCGTGGTTGCTG  
GTGGTGGGACGTCACTCGTGTGGTGTGTCATCATATACCACACAAGGGGAGGAATGAAGATTGCA  
AACACAGATGAGACCAACTGCCAGCAGATATTCTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGG  
GATGGGTACGTGTTCAAGAAAGTGGAGGCCACCAAGTGTGACATCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTC  
CTTGTCCGTTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGATCCTTTGAAACA  
TATCATAACAGGTGCACTGCCAGCAGATATTCTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGAC  
GAGTGTACCCATGTTCTCATCCTCAGAAGAAATCTGCAAGCAGGGAGGAATGAAGATTGCA  
GATGGGTACGTGTTCAAGAAAGTGGAGGCCACCAAGTGTGACATCTTCAGGTGCTGGATTTTCTTACCA  
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTC  
CTTGTCCGTTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGATCCTTTGAAACA  
TATCATAACAGGTGCACTGCCAGCAGATATTCTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGAC  
GAGTGTACCCATGTTCTCATCCTCAGAAGAAATCTGCAAGCAGGGAGGAATGAAGATTGCA  
GAAATCACATTGTACCTTAAACAGACTTAAAGAAACTACAGGACTCCAATTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGGAAAGCTTAAACATACTACCTCAAGTGAACCTTTATTAAAGAGAGA  
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAATTTTATCTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTA  
TTTATGCAAAAAGTATCTTACGTAATTATGATATAAATCATGATTATTGATTGTTATGATT  
TTTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT  
ACTCATTATATTGCACTTATATTAAATAAAATGTGCAATTGAAAAA  
AAAAAAAAAAAAA  
AAAAAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELQPSGVAERPCPTTCRCLGDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELRNKKINV DGLTFQGLGALKSLKMQR  
NGVTKLMGAFWG LSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAF RGLSSLKTL DLKNNEIS  
WTIEDMNGAFSGLDKLRLILQGNRIRSITKAFTGLDALEHLDLSDNAIMS LQGNAFSQM  
KLQLHLNTSSLLCDCQLKWLQPQWAENN FQSFVNASC AHPQLLKGRSIFA VSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMEN YAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLT VNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPP KLNWTKDDSPVVTERHF  
FAAGNQLLIIVDSVSDAGKYTC EMSNTLGTERGNVRLSVIPTPTCDSPQMTAPS LDDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDET NLPADIPS YLSSQGT LADRQ  
DGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD LFLCPFLGSTGP MY  
LKG NVYGSDFETYHTG CSPD PRTV LMDHYEPSYIKK ECP CSHP SEES CERSFSN ISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLEN YRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGGGAGAGCGCCAGCTGACTTGAAATGGAAGGGAGCCCCGAGCCCGGGAGCGCAGCTGAGAC  
TGGGGAGCGCGTTCGGCCTGTGGGCGCCCTCGCGCCGGGGCGCAGCAGGGAAAGGGAGCTGTTCTGCC  
CTGCTCCACAGGGCGCCACTGGTGTGAAACCGGGAGAGCCCCTGGTGGTCCCTCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGAGGGCTCATGGTGGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGGAGGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGTGTGC  
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGGAGGGCCCAAGGATTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCAAGAGAACGAATTGCGGAGGAGGCCGTGCTGGTACTGAGCCCTGAGG  
AGCCGGGCCTGGCCAGCCGCGTCAAGTGCCTGGAGACTGTGCTGTTCCAGGAGGGCGTGGACTGTG  
GCGGTATTGACCTGCGTGAGTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAACAAACCGCCTGA  
CTTCCCAGGGCTCCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTCCTGCCAACGCCCTGATCAGTGTGGACTTGCTGCCAACTATCTACCAAGATCT  
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTGACCTGCACAACAAACAAGCTGGCAGACGCCGGC  
TGCGGACAAACATGTTCAACGGCTCAGCAACGTCAGGCTCTCATCTGTCCAGCAACTCTCTGCCACGTGC  
CCAAGCACCTGCCCTGCCCTGTACAAGCTGCACCTCAAGAACAAACAAGCTGGAGAACGATCCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGAGCTACACTGAGAACAAACTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGGCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGCTCTGGGCTCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAACGCCCACCGGAGCCTGGAGCAGGGCATCCACCAACTGGCTTCCAGGGC  
GCAGCGCTGGAGTACCTGCTGCTGCACAGCAACAGCTGCGGGAGCAGGGCATCCACCAACTGGCTTCCAGGGC  
TCAAGCGGTTGACACCGTGCACCTGTACAACAAACGCGCTGGAGCGGTGCCAGTGGCCTGCCACGTG  
GCACCCCTCATGATCCTGCACAACCAAGATCACAGCATTGGCGCGAGACTTGGCACCACCTACTTCTGGAGG  
AGCTAACCTCAGTACAACCGCATCACAGCCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC  
GCTCGCTGGACTCTGCGGGCAACGGCTGCACACGCTGCCACCTGGCTGCCATGGAAATGTCATGTGCTGAAGG  
TCAAGCGAATGAGCTGGCTGCCCTGGCACAGCGCTGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCGAGCCCTGGGCCCCGTGCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA  
TCGCCGGAAATCAGTCACAGAGATCCCCGAGGGCTCCCGAGTCAGTGTGACTCTGAGTACCTGCAAGAACACA  
AGATTAGTGCGGTGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTACATTCCAAGGACCGTGGCGCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAACAAAGATGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC  
AGCACACGCCCTGTGCTGAGCCCCCACTCTGCCGTGCTCACACAGAACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTGCCACGGCTGCTCCACGGCCAGACACATGC  
ACACACATCACACCCCTAAACACCCAGCTGCCACACAAACTACCCCTCAAACCCACAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAGGGCTGCCCTGCCACACACAGGCACCCA  
TTCCCTCCCTGCTGACATGTGATGCTGATGCTACACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCCAAGCTATGCCACAGACAGCTTGGCCAGGCAATCAGCCATAGCAGCTGCCGTGCTGCC  
GTCCATCTGTCGGTCCGTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCACCCCT  
GGAACTCACAAAAGCTGGCTTTATTCCCTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGC  
TGGCCCACCTGCTCCCTGCCAGGTGCTGGCAGTCAGTGTCAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGACTTTCAATGGCAAGCCAGTGGAGGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGCCTGGGG  
CAGGAGTGAAGCAGAGGGTATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCTGTGGGGAGTTCCGGTGCCTTATTCTTATTCTAAGGAAAAAAATGATAAAAAAAT  
CTAAAGCTGATTTCTGTTATAGAAAACATAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFFEHTNLNYLYLANNK  
LT LAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ET FWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RVR TLMILHNQITGIGREDFATTYF  
LEELNLSYNRITS PQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLK GIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

GGGAGGGGGCTCGGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCCCTGCCGCTGTCCCTCGGGAGCGGGCAG  
CACTAGCCCAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCCCTCCCATCGCGCCACCACCC  
CAACCTGTTCTCGCGCCACTCGCTGCCAGGACCGCTGCCAACATGGATTTCCTGGCGCTGGT  
GCTGGTATCCTCGCTCACCTGCAGGCGGCCAGTCAGGGAGGTGGCCAGGCAAATAGTGTATCGAT  
TGGCTATGTCGTTATGGTGGAGGATTGACTGCTGCTGGGCTGCCAGTCTGGGACAGTGTAGCC  
TGTGCCAACCACGATGCAAACATGGTAATGTATCGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGCCCTGTAAGCACAGGTGCATGAACACTTA  
CGGAGCTACAAGTGTACTGTCACCGATATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACGTCACTGGCTGTGATGTTAAAGGACAAATACGGGCCAGTGCCATCCCTGGCCT  
GCACCTGGCTCTGATGGAGGACCTGTGAGATGTGCTACAGGAAGAGCCTCTGCCCTAGATT  
TAGGCAATGTCACACTTGGAGCTACATCTGCAAGTGTATGCTAAAGGCTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCACTGTCAGTATCAGTGAGCAGCTTGCTCGATGTTATAA  
CGTACGGGCTCTAACAGTCAAAGTAAAGAAGGATACCAGGGTGTGGACTGACTTGTGTATATCCAAA  
AGTTATGATGAAACCTCAGGTCATTGACAAAGGAAATGGTACCAATTAAAGGGTGAACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAACTTGGTGGCTCCGAAGACACCATATATTCTCTATCATTACCAA  
CAGGCCTACTTCTAACAGCAACACAAGACCTACACCAAAGCCAACACCAATTCTACTCCACCAACCCACC  
CCTGCCAACAGAGCTCAGAACACCTCTACCCACTACAACCCAGAAAGGCCAACCCGACTGACAACATAGC  
ACCACTGCCAGTACACCTCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACACCTCAGAAACCCAGAGG  
AGATGTGTCAGTGTCTGGTACACAGTTGTAATTTGACCATGGACTTTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACGGAAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCCAAGCCCCAGG  
GGGAAAGCTGCACGCTGGTGTACCTCTGGCCCTCATGCAATTGGGACCTGTGCTGTGATTAGGCA  
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCCACGGAGCAGCCCTGTG  
GGGAGAAATGGTGGCATGGTGGAGGCAAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCAATCACA  
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAATGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGGAAACCAATTGATGGTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGGACAGCTG  
TTCTCCATATGCACTAACAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG  
GCCATTGTTAGAATACTCTAACAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAATTAGA  
TAAAAATTGCTATTAAGATGGTAAAGATGTTACCCAAGGAAAAGTAACAAATTATAGAATTCCCAA  
AGATGTTTGATCCTACTAGTGTGCACTGAGTAAATCTTACAATAATTGGACAAGGCTTAATTAGG  
CATTCCCTTGACCTCTAACGGAGGGATTGAAAGGGGAAGAGGCCACAAATGCTGAGCTACTGAAATA  
TCTCTCCATTGGCAATTCTAGCAGTATTAAAGAAAAAGAAACTATTATCCAAATGAGAGTATGATGGAC  
AGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTAGATTGTTCAAGATTGTTTAAGAGATCCTCAAGGAACACAGTTCAGAGAG  
ATTTCATCGGGTGCATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC  
ACACCGGCAGACCTTCTCACCTCATCAGTATGATTCAAGTTCTTCAATTGGACTCTCCAGGGTCCAC  
AGAACAGTAATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGTAAGGCAGGGCTGG  
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTGTTAATGGTTCATT  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTGTTACTTGTGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT  
CTAAAATAAAAATGTTAGTGTGTTCCAAATGGCCTAATAAAAACAATTATGTAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDL MYI GGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKC EGYQG  
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA A ST PPGGITVDN  
RVQTDPQKPRGDVF SVLVHSCNF DHGLCGWI REKDNDLHW EPI RDPA GGQYLTV SAAKA PGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGA HGA ALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTCACAACTTCCCTTCCTTGCAACAGGTGCTGCTGGGGCTGA**  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA  
ACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGAACTCTATGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGAGATTCATCCTCCCT  
CTGGGCTGTGGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTAGGAACCCGTCAAGTGAATGAAAGTGATATCATTATGCCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTGTTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGTTACAACAAACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTACATCACTTCCGTAGGACTGGAGAAGCTG  
CACAGAAAGGAAAATCATTGTCACCTTCTAGCAAGTATAACTGGAATATCACTATTGATT  
ATATCCATGTGCTTCTCTTCTATGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGAATATATGAATTGTTCTCAGATGTTCTGGTGTGTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAG**TGA**ACTTCTG  
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATTCTTTACA  
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTCTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTCTTCAAAATTCTATCTTGTGTTATTGTACAA  
CAAAGTAATAAGGATGGTTGTACAAAAACAAACTATGCCCTCTCTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGTGTTAAAAAAAAAAAAAA

## FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNNTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPRSVPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGC~~AA~~**A**TGGCCCTCCGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCTCCCTGGACGCACGGCGGCGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGGAGAAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCTACTATTTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG  
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGACTGTTATTAGGACTCTGTATGATATTGTG  
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAACATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCCT**AG**TAAATTATAG  
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGATAATTGCAAGGTTCACTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGCAGTATGATG  
GTTAAATAGTTCTCTAATTGAAAAATCGTCCAAGCAATAAGATTATGATATTG  
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCATTAT  
TGAGGTATTAAAGAAGATTATTAGAGAAAATATTCTCATTTGATATAATTGTTCTCTG  
TTCACTGTGTGAAAAAAAGAAGATATTCCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTATTCACTGACAATTCTGGTCTTTAGAGGTATTCCAAAATTCTCTGT  
ATTAGTTAGGTTATGCAACTAAACACTACCTTACATTAATTAAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCACTGGTATTCTCTGATT  
CAACAAAGTTGATTCTCTGTATTCTACTATGGTTACATTTTATT  
CAAATTGGATGATAATTCTGGAAACATTGTTATGTTTAGAAACAGTATTGTT  
GTTCAAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATTAAATT  
TTGCCACTTTTCAGATTACATCATTCTGCTGAATTCAACTTGAAATTGTT  
TTCTTTGGATGTGAAGGTGAACATTCTGATTGATGTGAAAAGCCTGGTA  
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG  
CATCTCTGTATATGCTTAAATGTATTGTCCTCATACAGAAAGTTCTAATTGAT  
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATTAAAAGACAA  
ACTCATATTATCCTGTTCTTCTGACTGGTAATTGTTGGGATTCACAGGTAAA  
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTTAAAGAGCTAGAATACATAGTTT  
CACCTTAAAGAAGGGGAAATCAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTCTGTAATGCCCCCTTCTAGGCTCTGCTGTGAATTGATTAGATTACAG  
TATCGTAATATAAGTTCTTAAAGCCCTCTCTAGAATTAAATATTGTACCA  
AAAGAGTTGGATGTGTAATTGATGCCTTAGAAAAATACCTAACAGCACAAATAAACCT  
TTCTAACCACTTCATTAAGCTGAAAAA

## FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCAGGATTGGAAGAGCGGG  
AAGGTCTGGCCAGAGCAGTGTGACACTTCCTCTGTGACC**ATGAA**ACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGACAGGCCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTACCCCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCAGGCTACCTGGCTACCCCTGTGAATGCCTACAAACTGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGGCTCACCCGCCCTGCTC  
TCCCTTGACCCAAGGCCACGAACGAGCTGGAGGGAATCTCGGTACTTGTAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG  
GAGGGTGTCAAACGTACACCCCCGTAGACAGAAAGAGGCTTCTGTAGGTACCAACCATTGCAA  
CAGGGCCCCACAGCTGCTATTGCCCTCAAAGAGGAGGAGGAGTGGGACAGCCCGACA  
TCGTCAGGTACTACGATGTATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGAAAAA  
CCTAAACTTGACGCCACCGTCTGTGATCCAAGACAGGAGTCCTCACTGTCGCCAGCTA  
CCGGGTTCCAAAAGCTCTGGTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCCACTTCGACTTCTCTAGGCGACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTGTGGATCAACAGAAGTTGACT**TGA**CATCCTTCTGTCTTCCCTGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTCATTCAAGCCTGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAATGTCCTACCAAGAAAAAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEATTTKSQVLDYLSYAVFQLGDLHRALELTTRLLSLDPHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEGVKLTPRRQKRLF  
CRYHHGNRAPQOLLIAPFKEEDEWDSPHIIVRYYDVMSDDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSR  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTCCCTCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT  
TTCATTATTACCGTTTGGCTGGGGTAGTCCGACACCTCACAGTTGAAGAGCAGGCCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTTGGGGATGCTGGCTCTGGAAAGCAGCGGGCTTGCTCTGTCTTGGCCTCATGACCC  
CAGGTTCTCTGGTAAAACGTAAAGCCTACTAGGCCTGGTGCCTCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGCAGGGCCTACCAACCATGCGACTGAGCTCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTAGGGCTGCTCTGGGTGCAGCCTGAGCCTCTGCCGGTTCTGGATCCAGGGGAGGGAGAAAG  
ATCCCTGTGAGGCTAGGGGAGCAGGAGGGCCACAGAACATCCAGATTGAGAGCTGGCTAGACCAAAGTG  
ATGAAGACTTCAACCCCCGGATTGCCCCTACTACAGGGACCCCAACAAGCCCTACAAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCTCCGTGAGCGGTTGCTGGCTGTGACCTCCCAGCTACACTGTCCA  
CTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGTTACTCTACTTCACGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGGCGACTACGACTGGTCTTCATCATGCAGGATGACACATATGTGAGGCC  
CCGCCTGGCAGCCCTGCTGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATGG  
GCGAGCGAGCAGGCCGGTACTGTCATGGGGCTTGGTACCTGTTGTCAGGAGTCTCTGCTCGTCTGC  
GGCACATCTGGATGGCTGCCAGGAGACATTCTCAGTGCCCTGACGAGTGGCTGGACGCTGCCATTG  
ACTCTCTGGCGCTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACTGGCAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTGGTTCTGAGTGCCTCGCCGTGACCCCTGTCCTCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTGGAGCGGGTTACAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGAACCTGACCGTGTGACCCCCGAAAGGGGAGGCAGGGCTGAGCTGGCCCTGGGCTCCTGCTCCTTCA  
CACACACTCTCGCTTGAGGTGCTGGCTGGACTACTTCACAGGAGCAGCACCTCTCCTGTGAGATGGG  
CTCCAAGTGCCACTACAGGGGCTAGCAGGGGAGCTGGTGTGAGCTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTGCCCTTCAAGACAGGAGCTGCTCAACGGCTATGGCGCTTCGACCCAGCAC  
GGGCATGGAGTACACCTGGACCTGTTGGAATGTTGACACAGCGTGGCACCGGGCCCTGGCTCGCA  
GGTCAGCCTGCTGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGTGCAACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCCGTGAGCAATGTC  
TGGAGCCACGAGAACATGCAATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG  
ACCCATTCTGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGGGTACCCCTGGACGAGGCTGGCTGGCTCG  
CTGCGAGCAGAGGCCCTTCCAGGTGCAGACTCATGGACGTGGCTCGAAGAACGACCCCTGTGGACACTCT  
TCTCCTTACCAACCGTGTGGACAAGGCCTGGGCCAGTCTCAACCGCTGCGCATGAATGCCATCTCTGGCT  
GGCAGGCCCTTTCCAGTCCATTCCAGGAGTTCAATTCTGCCCTGTCACACAGAGATCACCCCAAGGGCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTTCTGCGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCTCGGTTCTCAGGGCTCC  
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCCGTGCCCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGCCCTAACCTATTACCTTCTGTGCTGCCCTCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAACATTGTTGCTGTATTAAATGAAATGTTATTAA  
ACATGTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGPQNPDZRARLD  
QSDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETRHLHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRC  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFAAANVLEPREHALLTLVYGPREGGRGAPDPFLGVKA AAAAELEERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTWTRPGPEVLRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQEQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCCGTGCGCGCTGC~~G~~CTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACAAACACTGTGACAAAGCAG  
AGTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA~~ACT~~G  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAAGATGCTGATGG  
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTAGATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTAGGCATTGGCATATTCAAT  
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGAGTAGTAACATACATACCAA  
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTCTTAAACACATGAACATTGTAAATG  
TGGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGGAAAAT

## FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 121

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCCGCCACCGGCAC  
TCCGGCTCTGGCTCGCTGACTTCTTCCTGCTGCTGCTTCAAGGGCTGCCTGATAGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCACTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG  
AGACAAGTGACCCCAAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGCGAGAAATCTGGGGAAAGACATCCCTGAAGATCTGGATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTA  
CTGTCAGTGAAAGCCAGTGCACCCCTGTCTGTAGAGTGGCGAAGGCTGTACAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCCCGCCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCGAATTCTTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTTCACTGCTG  
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGGTCTGGTTGCTCTGTACTGGCCCTG  
TCACGTTGGCATCTGCTGTGCATAACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTCAGACACAAGTCATGTTTG  
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGACATACTCTGCTAGAAACTCCGTCAA  
GGCAGCAGAGAGCTGATGCACTGGACAGAGCTAGACACTCATTAGAAGCTTTCGTTTGGCAAAGTTGACCA  
CTACTCTCTTACTCTAACACAGCCATGAATAGAAGAATTTCCTCAAGATGGACCCGGAAATAACACAA  
GGAAGCGAAACTGGGTGCGTCACTGAGTTGGTCTTAATCTGTTCTGGCTGATTCCGCATGAGTATTAGG  
GTGATCTAAAGAGTTGCTCACGTAACAGCCGTCTGGCCCTGTGAAGGCAGCATGTCACCACGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA  
GAAAAGGCTCTTACACAGCAGCCTTACTTCATGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGAGTTGGAGAAGCTTTTGATCAGCATTGTAAGGAAACACAAACAAAATCAGGAAG  
GTAATTGGTGCTGAGAGGGATCTGCTGAGGAACCTGCTTGTCAAACAGGGTGTCAAGGATTAAAGGAAA  
ACCTCTGCTTAAAGCTGAAATGGTACTGAAATGCTTTCTATGGGCTCTGTTATTAAACACAAAC  
TACATCTAAATTGGCTAAGGATGTTGGATTATTGAAAAGAAAATTCTATTAAACTGTAATATTGTT  
CATACAATGTTAAACACTTTTAAAGGTTCAACTTAAGGTTAGAAGTCAAGCTACTAGTGTAAAT  
TGGAAAATCTAATAATTAAAGGTTGGCAACTTACCAAGGAATCCTCTATGGAAGTTACTGTTGATGTTCTTCT  
CACACAAGTTTACGGCTTCAAGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATCCAGTTAAGCAATGTTGAAATCAGTTGCATCTTCAAAAGAAACCTCTCAGGTTAGCTTGA  
GCCTCTCTGAGATGACTAGGACAGTCTGTAACCCAGGGCCACCCAGAAGCCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGGTGCAGCGCCAGGGCCCCGCTCTAGCTACTGTTGCTCGTCTGCCAGGAGGCC  
GCCATCCTGGCCCTGGCAGTGGCTGTCCAGTGAGCTTACTCAGTGGCCCTGCTCATCCAGCACAGC  
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT  
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTTTTTAAAGTTGTTATTGGAT  
AAGATTGCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAGTACAATAACATTAAAGAAAATGGAT  
CCCACGTCTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTCAAACAAACCATGAT  
GGAGTGGCGCCAGTCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGAGGAAAG  
TGAAACGCCGAATCAAAGCAGTTCTAATTGACTTTAAATTCTATCCGCCGGAGACACTGCTCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTTCACTGTTGCT  
GAATGGCTCTCACTACTCACCTGTTCTTCAGCTTCCAGGTGCTTGGTTTATACTTGAAGCTTTTT  
AATGCAATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGCCAGGGCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATGCCACCTTGGTAGAGAGGGATGGCTCCACCTCAGCAGGGGATTACGCTCCAGCCTC  
TCTGGTTGTCATAGTGTAGGGTAGCTTATTGCCCTCTTCTATACCCCTAAACCTTCTACACTAGTCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGAGTAGCTGCCATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACAGGGCTGTGATTCT  
GCCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTATAAAAGCTTCAAAAAACCA

## FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTCPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAVRGGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267